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RAW SEQUENCE LISTING  
 PATENT APPLICATION: US/09/381,286A

DATE: 01/09/2003  
 TIME: 11:47:27

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Input Set : A:\15649039.app  
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3 <110> APPLICANT: GROLL, MICHAEL  
 4 HUBER, ROBERT  
 5 DITZEH, LARS  
 6 ENGH, RICHARD  
 8 <120> TITLE OF INVENTION: PROCESS FOR THE PURIFICATION AND CRYSTALLIZATION OF  
 9 PROTEASOME  
 11 <130> FILE REFERENCE: 100564-09039  
 13 <140> CURRENT APPLICATION NUMBER: 09/381,286A  
 C--> 14 <141> CURRENT FILING DATE: 1999-12-17  
 16 <150> PRIOR APPLICATION NUMBER: PCT/EP98/01653  
 17 <151> PRIOR FILING DATE: 1998-03-20  
 19 <150> PRIOR APPLICATION NUMBER: EPO 97104877.2  
 20 <151> PRIOR FILING DATE: 1997-03-21  
 22 <160> NUMBER OF SEQ ID NOS: 14  
 24 <170> SOFTWARE: PatentIn Ver. 2.1  
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 27 <211> LENGTH: 203  
 28 <212> TYPE: PRT  
 29 <213> ORGANISM: Thermoplasma acidophilum  
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 35 Glu Arg Arg Val Thr Met Glu Asn Phe Ile Met His Lys Asn Gly Lys  
 36 20 25 30  
 38 Lys Leu Phe Gln Ile Asp Thr Tyr Thr Gly Met Thr Ile Ala Gly Leu  
 39 35 40 45  
 41 Val Gly Asp Ala Gln Val Leu Val Arg Tyr Met Lys Ala Glu Leu Glu  
 42 50 55 60  
 44 Leu Tyr Arg Leu Gln Arg Arg Val Asn Met Pro Ile Glu Ala Val Ala  
 45 65 70 75 80  
 47 Thr Leu Leu Ser Asn Met Leu Asn Gln Val Lys Tyr Met Pro Tyr Met  
 48 85 90 95  
 50 Val Gln Leu Leu Val Gly Gly Ile Asp Thr Ala Pro His Val Phe Ser  
 51 100 105 110  
 53 Ile Asp Ala Ala Gly Gly Ser Val Glu Asp Ile Tyr Ala Ser Thr Gly  
 54 115 120 125  
 56 Ser Gly Ser Pro Phe Val Tyr Gly Val Leu Glu Ser Gln Tyr Ser Glu  
 57 130 135 140  
 59 Lys Met Thr Val Asp Glu Gly Val Asp Leu Val Ile Arg Ala Ile Ser  
 60 145 150 155 160  
 62 Ala Ala Lys Gln Arg Asp Ser Ala Ser Gly Gly Met Ile Asp Val Ala  
 63 165 170 175  
 65 Val Ile Thr Arg Lys Asp Gly Tyr Val Gln Leu Pro Thr Asp Gln Ile

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75 <213> ORGANISM: Saccharomyces cerevisiae
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81 Gly Lys Asp Cys Val Ala Ile Ala Cys Asp Leu Arg Leu Gly Ser Gln
82          20          25          30
84 Ser Leu Gly Val Ser Asn Lys Phe Glu Lys Ile Phe His Tyr Gly His
85          35          40          45
87 Val Phe Leu Gly Ile Thr Gly Leu Ala Thr Asp Val Thr Thr Leu Asn
88          50          55          60
90 Glu Met Phe Arg Tyr Lys Thr Asn Leu Tyr Lys Leu Lys Glu Glu Arg
91   65          70          75          80
93 Ala Ile Glu Pro Glu Thr Phe Thr Gln Leu Val Ser Ser Ser Leu Tyr
94          85          90          95
96 Glu Arg Arg Phe Gly Pro Tyr Phe Val Gly Pro Val Val Ala Gly Ile
97          100          105          110
99 Asn Ser Lys Ser Gly Lys Pro Phe Ile Ala Gly Phe Asp Leu Ile Gly
100          115          120          125
102 Cys Ile Asp Glu Ala Lys Asp Phe Ile Val Ser Gly Thr Ala Ser Asp
103          130          135          140
105 Gln Leu Phe Gly Met Cys Glu Ser Leu Tyr Glu Pro Asn Leu Glu Pro
106 145          150          155          160
108 Glu Asp Leu Phe Glu Thr Ile Ser Gln Ala Leu Leu Asn Ala Ala Asp
109          165          170          175
111 Arg Asp Ala Leu Ser Gly Trp Gly Ala Val Val Tyr Ile Ile Lys Lys
112          180          185          190
114 Asp Glu Val Val Lys Arg Tyr Leu Lys Met Arg Gln Asp
115          195          200          205
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120 <212> TYPE: PRT
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127 Ser Ser Lys Ala Val Thr Arg Gly Ile Ser Val Leu Lys Asp Ser Asp
128          20          25          30
130 Asp Lys Thr Arg Gln Leu Ser Pro His Thr Leu Met Ser Phe Ala Gly
131          35          40          45
133 Glu Ala Gly Asp Thr Val Gln Phe Ala Glu Tyr Ile Gln Ala Asn Ile
134          50          55          60
136 Gln Leu Tyr Ser Ile Arg Glu Asp Tyr Glu Leu Ser Pro Gln Ala Val
137 65          70          75          80

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139 Ser Ser Phe Val Arg Gln Glu Leu Ala Lys Ser Ile Arg Ser Arg Arg
140      85                      90                      95
142 Pro Tyr Gln Val Asn Val Leu Ile Gly Gly Tyr Asp Lys Lys Lys Asn
143      100                      105                      110
145 Lys Pro Glu Leu Tyr Gln Ile Asp Tyr Leu Gly Thr Lys Val Glu Leu
146      115                      120                      125
148 Pro Tyr Gly Ala His Gly Tyr Ser Gly Phe Tyr Thr Phe Ser Leu Leu
149      130                      135                      140
151 Asp His His Tyr Arg Pro Asp Met Thr Thr Glu Glu Gly Leu Asp Leu
152 145                      150                      155                      160
154 Leu Lys Leu Cys Val Gln Glu Leu Glu Lys Arg Met Pro Met Asp Phe
155      165                      170                      175
157 Lys Gly Val Ile Val Lys Ile Val Asp Lys Asp Gly Ile Arg Gln Val
158      180                      185                      190
160 Asp Asp Phe Gln Ala Gln
161      195
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165 <211> LENGTH: 222
166 <212> TYPE: PRT
167 <213> ORGANISM: Saccharomyces cerevisiae
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173 Gly Glu Asp Phe Ala Val Leu Ala Gly Asp Thr Arg Asn Ile Thr Asp
174 20 25 30
176 Tyr Ser Ile Asn Ser Arg Tyr Glu Pro Lys Val Phe Asp Cys Gly Asp
177 35 40 45
179 Asn Ile Val Met Ser Ala Asn Gly Phe Ala Ala Asp Gly Asp Ala Leu
180 50 55 60
182 Val Lys Arg Phe Lys Asn Ser Val Lys Trp Tyr His Phe Asp His Asn
183 65 70 75 80
185 Asp Lys Lys Leu Ser Ile Asn Ser Ala Ala Arg Asn Ile Gln His Leu
186 85 90 95
188 Leu Tyr Gly Lys Arg Phe Phe Pro Tyr Tyr Val His Thr Ile Ile Ala
189 100 105 110
191 Gly Leu Asp Glu Asp Gly Lys Gly Ala Val Tyr Ser Phe Asp Pro Val
192 115 120 125
194 Gly Ser Tyr Glu Arg Glu Gln Cys Arg Ala Gly Gly Ala Ala Ala Ser
195 130 135 140
197 Leu Ile Met Pro Phe Leu Asp Asn Gln Val Asn Phe Lys Asn Gln Tyr
198 145 150 155 160
200 Glu Pro Gly Thr Asn Gly Lys Val Lys Lys Pro Leu Lys Tyr Leu Ser
201 165 170 175
203 Val Glu Glu Val Ile Lys Leu Val Arg Asp Ser Phe Thr Ser Ala Thr
204 180 185 190
206 Glu Arg His Ile Gln Val Gly Asp Gly Leu Glu Ile Leu Ile Val Thr
207 195 200 205
209 Lys Asp Gly Val Arg Lys Glu Phe Tyr Glu Leu Lys Arg Asp
210 210 215 220

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222 Asp Asn Gly Val Ile Ile Ala Ala Asp Asn Leu Gly Ser Tyr Gly Ser
223               20               25               30
225 Leu Leu Arg Phe Asn Gly Val Glu Arg Leu Ile Pro Val Gly Asp Asn
226               35               40               45
228 Thr Val Val Gly Ile Ser Gly Asp Ile Ser Asp Met Gln His Ile Glu
229   50               55               60
231 Arg Leu Leu Lys Asp Leu Val Thr Glu Asn Ala Tyr Asp Asn Pro Leu
232   65               70               75               80
234 Ala Asp Ala Glu Glu Ala Leu Glu Pro Ser Tyr Ile Phe Glu Tyr Leu
235               85               90               95
237 Ala Thr Val Met Tyr Gln Arg Arg Ser Lys Met Asn Pro Leu Trp Asn
238               100              105              110
240 Ala Ile Ile Val Ala Gly Val Gln Ser Asn Gly Asp Gln Phe Leu Arg
241               115              120              125
243 Tyr Val Asn Leu Leu Gly Val Thr Tyr Ser Ser Pro Thr Leu Ala Thr
244   130              135              140
246 Gly Phe Gly Ala His Met Ala Asn Pro Leu Leu Arg Lys Val Val Asp
247 145              150              155              160
249 Arg Glu Ser Asp Ile Pro Lys Thr Thr Val Gln Val Ala Glu Glu Ala
250               165              170              175
252 Ile Val Asn Ala Met Arg Val Leu Tyr Tyr Arg Asp Ala Arg Ser Ser
253               180              185              190
255 Arg Asn Phe Ser Leu Ala Ile Ile Asp Lys Asn Thr Gly Leu Thr Phe
256               195              200              205
258 Lys Lys Asn Leu Gln Val Glu Asn Met Lys Trp Asp Phe Ala Lys Asp
259   210              215              220
261 Ile Lys Gly Tyr Gly Thr Gln Lys Ile
262 225              230
265 <210> SEQ ID NO: 6
266 <211> LENGTH: 232
267 <212> TYPE: PRT
268 <213> ORGANISM: Saccharomyces cerevisiae
270 <400> SEQUENCE: 6
271 Thr Thr Ile Val Gly Val Lys Phe Asn Asn Gly Val Val Ile Ala Ala
272   1               5               10               15
274 Asp Thr Arg Ser Thr Gln Gly Pro Ile Val Ala Asp Lys Asn Cys Ala
275               20               25               30
277 Lys Leu His Arg Ile Ser Pro Lys Ile Trp Cys Ala Gly Ala Gly Thr
278               35               40               45
280 Ala Ala Asp Thr Glu Ala Val Thr Gln Leu Ile Gly Ser Asn Ile Glu
281   50               55               60
283 Leu His Ser Leu Tyr Thr Ser Arg Glu Pro Arg Val Val Ser Ala Leu

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284 65          70          75          80
286 Gln Met Leu Lys Gln His Leu Phe Lys Tyr Gln Gly His Ile Gly Ala
287          85          90          95
289 Tyr Leu Ile Val Ala Gly Val Asp Pro Thr Gly Ser His Leu Phe Ser
290          100          105          110
292 Ile His Ala His Gly Ser Thr Asp Val Gly Tyr Tyr Leu Ser Leu Gly
293          115          120          125
295 Ser Gly Ser Leu Ala Ala Met Ala Val Leu Glu Ser His Trp Lys Gln
296          130          135          140
298 Asp Leu Thr Lys Glu Glu Ala Ile Lys Leu Ala Ser Asp Ala Ile Gln
299 145          150          155          160
301 Ala Gly Ile Trp Asn Asp Leu Gly Ser Gly Ser Asn Val Asp Val Cys
302          165          170          175
304 Val Met Glu Ile Gly Lys Asp Ala Glu Tyr Leu Arg Asn Tyr Leu Thr
305          180          185          190
307 Pro Asn Val Arg Glu Glu Lys Gln Lys Ser Tyr Lys Phe Pro Arg Gly
308          195          200          205
310 Thr Thr Ala Val Leu Lys Glu Ser Ile Val Asn Ile Cys Asp Ile Gln
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313 Glu Glu Gln Val Asp Ile Thr Ala
314 225          230
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319 <212> TYPE: PRT
320 <213> ORGANISM: Homo sapiens
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327          20          25          30
329 Lys Ile His Phe Ile Ala Pro Lys Ile Tyr Cys Cys Gly Ala Gly Val
330          35          40          45
332 Ala Ala Asp Ala Glu Met Thr Thr Arg Met Val Ala Ser Lys Met Glu
333          50          55          60
335 Leu His Ala Leu Ser Thr Gly Arg Glu Pro Arg Val Ala Thr Val Thr
336 65          70          75          80
338 Arg Ile Leu Arg Gln Thr Leu Phe Arg Tyr Gln Gly His Val Gly Ala
339          85          90          95
341 Ser Leu Ile Val Gly Gly Val Asp Leu Thr Gly Pro Gln Leu Tyr Gly
342          100          105          110
344 Val His Pro His Gly Ser Tyr Ser Arg Leu Pro Phe Thr Ala Leu Gly
345          115          120          125
347 Ser Gly Gln Asp Ala Ala Leu Ala Val Leu Glu Asp Arg Phe Gln Pro
348          130          135          140
350 Asn Met Thr Leu Glu Ala Ala Gln Gly Leu Leu Val Glu Ala Val Thr
351 145          150          155          160
353 Ala Gly Ile Leu Gly Asp Leu Gly Ser Gly Gly Asn Val Asp Ala Cys
354          165          170          175
356 Val Ile Thr Lys Thr Gly Ala Lys Leu Leu Arg Thr Leu Ser Ser Pro

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**VERIFICATION SUMMARY**

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